

Application No. 10/763,502
Response dated August 15, 2007, 2007
Reply to March 15, 2007 Office Action

Exhibit A



Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

Taxonomy

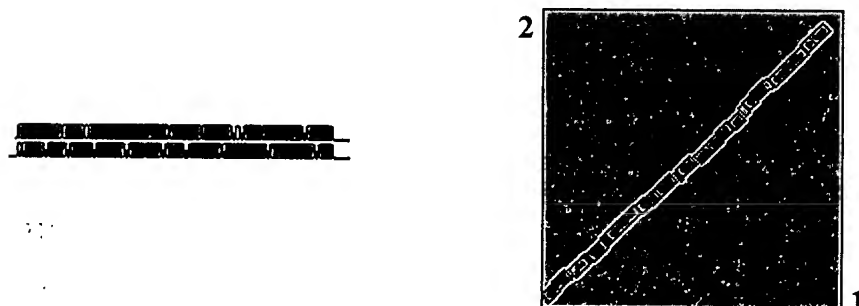
Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.16 [Mar-25-2007]

Matrix **BLOSUM62** gap open: **11** gap extension: **1**
 x_dropoff: **0** expect: **10.0000** wordsize: **3** Filter ☒ View option **Standard**
 Masking character option **X for protein, n for nucleotide** Masking color option **Black**
☐ Show CDS translation **Align**

Sequence 1: lcl|seq_1(C. elegans PAMP - SEQ ID NO:12)
 Length = 720 (1 .. 720)

Sequence 2: lcl|seq_2(Mouse PAMP - SEQ ID NO:16)
 Length = 708 (1 .. 708)



NOTE: Bitscore and expect value are calculated based on the size of the nr database.



Score = 160 bits (405), Expect = 5e-37

Identities = 154/701 (21%), Positives = 291/701 (41%), Gaps = 83/701 (11%)

Query	9	LIIAGIRCDGFSQVFRTLFIGEGNACYRTFNKTHEFGCQANRENENGLIVRIDKQEDFK	68
		+++AG+ C G S + + + + C R N TH+ GCQ++ + G+I ++K+ED K	
Sbjct	24	VVLAGL-CGGNSVERKIYIPLNKTAPCVRLNATHQIGCQSSISGDTGVIHVVEKEEDLK	82
Query	69	NLDSCWNSFYPKYSGKYWALLPVNLIRRDITISQLKSSKC-LSGIVLYNSGESIHPGDEST	127
		W + Y LL L RD + +LK + ++G+ + ++ + ++	
Sbjct	83	-----W-VLTDGPNPPYMLLEGKLFTRDVMKLGTTTSRIAGLAV-----TLAKPNSTS	131
Query	128	AASHDAECPNAASDYLLQDKNEEY--CERKI-NSRGAITRDGLMKIDWRIQMVFIDNSTD	184
		+ S +CPN Y E+ C++ + N G +GL D+ + +++ +	
Sbjct	132	SFSPSVQCPNDGFGIYSNSYGPEFAHCKKTLWNLG---NGLAYEDFSFPIFILLEDENE	187
Query	185	LEIIIEKCYSMFNKPKEDGSSGYPCGMSFRLANMAAGNSEICYRRGKNDAKLFQMNIDSG	244
		++I++CY N + + +P C M A ++ C RR F + S	
Sbjct	188	TKVIKQCYQDHNLGQNGSAPSFFLCAMQLFSHMHAVISTATCMRRS-----FIQSTFSI	241

```
Query 245 DAPQLCGAMHSDNIFAFPTPIPTSPNETIITSKYMMVTARMDSFSGMPEISVGEVSVLT 304
+ +C + N+++ PI TS E + + ++ R+DS ++ G S +
Sbjct 242 NPEIVCDPLSDYNVWSMLKPINTSVGLEPDV--RVVVAATRLDSRSFFWNVAPGAESAVA 299

Query 305 SIISVLAAARSMGTQIEKWQKASN--TSNRNVFFAFFNGESLDYIGSGAAAYQMENGKFP 362
S ++ LAAA ++ KA + T +RNV F FF GE+ DYIGS Y MENGKF
Sbjct 300 SFVTQLAAAEAL-----HKAPDVTTLSRNVMFVFFQGETFDYIGSSRMVYDMENGKF- 351

Query 363 QMIRSDRTHIHPIRPNELDYILEVQQIGVAKGRKYYVHVD--GERYQQNKQTQDRVIDRI 420
P+R +D +E+ Q+ + ++H D ++ + K Q + ++ +
Sbjct 352 -----PVRLNIDSFVELGQVALRTSLDLWMHTDPM SQKNESVKNQVEDLLATL 400

Query 421 ERGLRSHAFDLEKPSGSGDRVPPASWHSFAKADAHVQSVLLAPYGKEYEYQRVNSILDK- 479
E+ + + +PP+S F +A ++ V+LA + + + SI D
Sbjct 401 EKSGAGVPEVVLRRLAQS QALPPSSLQRFLRA-RNISGVVLADHSGSFHNRYQSIYDTA 459

Query 480 -----NEWTEDE-----KAIQEIEAVSTAILAAAADYVGVETDEVVAKVDKKLITT 527
EW E + + + V+T + A + G + D + +T
Sbjct 460 ENINVTYPEWQSPPEEDLNFVTD TAKALANVATV LARALYELAGGTNFSSSIQADPQTVTR 519

Query 528 IFDCLI--TSNFWFDCDFMQKLDGGRYHKLFSYGFNQKSTYISMESHTAFPTVLHWLTI 585
+ + +N WF H L + YI++ S T V+ +
Sbjct 520 LLYGFLVKANNSWFQSILK-----HDLRSYDDRPLQHYIAVSSPTNTTYVVQYALA 571

Query 586 FALGSDKETLNVKSEKSCSHLGQFQAMYTYTWQPNPYTGNFS-----CLKSAIVKKVMVS 640
G + + + +Y Y+W P+ N + C++S + +S
Sbjct 572 NLTGKATNLTREQCQDPSKVPNESKDLYEYSWVQGPWNSNRTERLPQCVRSTVRLARALS 631

Query 641 PAVDSQTPEEEMNTRYSTWMESVYIIESVNLYLMEDASFHEY 681
PA + + +T YSTW ES + ++L+ E+
Sbjct 632 PAFEL---SQWSSTEYSTWAESRWKDIQARIFLIASKKLEF 669
```

CPU time: 0.03 user secs. 0.01 sys. secs 0.04 total secs.



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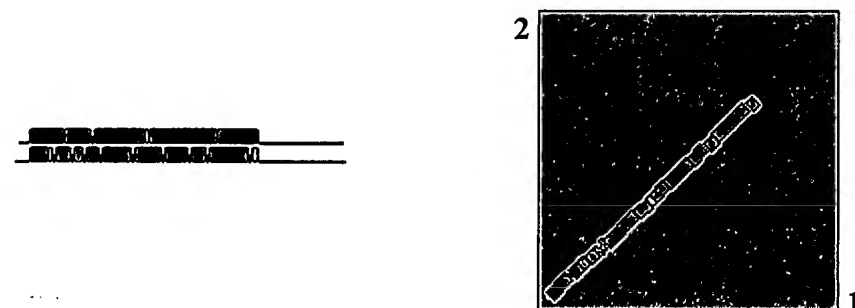
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 Masking character option **X for protein, n for nucleotide** ☒ Masking color option **Black** ☒
☐ Show CDS translation **Align**

Sequence 1: lcl|seq_1(C. elegans PAMP - SEQ ID NO:12)
 Length = 720 (1 .. 720)

Sequence 2: lcl|seq_2(D. melanogaster PAMP - SEQ ID NO:18)
 Length = 695 (1 .. 695)



NOTE:Bitscore and expect value are calculated based on the size of the nr database.



Score = 115 bits (288), Expect = 2e-23

Identities = 116/501 (23%), Positives = 210/501 (41%), Gaps = 62/501 (12%)

Query	32	GNACYRTFNKTHEFGCQANRENENGLIVRIDKQEDFKNLDSCWNSFYPKYSGKYWALLPV	91
		G +C+R N TH+ GC + G++ I+ + D + L S S P Y+ ++P	
Sbjct	37	GASCFRRLNGTHQTGCSSTYSGSVGLHLINVEADLEFLLSSPPS--PPYA----PMIPP	90
Query	92	NLIRRDITISQLKSS--KCLSGIVLYNSGESIHGDESTAASHDAECPNAASDYLLQDKNE	149
		+L R+ + +LK + K +S ++L N ++ SH+ CPN S +	
Sbjct	91	HLFTRNNLMRLKEAGPKNISVLLINRT-----NQMKQFSHELNCNPQYSGL---NSTS	141
Query	150	EYCE-----RKINSRGAITRDGLMKIDWRIQMVFIDNSTDLIIEKCYSMFNKPKEDGSS	204
		E C+ + N G GL+ D+ + +I + + +EKC+ FN + +	
Sbjct	142	ETCDASNPAKNWNPWGT----GLLHEDFFPIYYIADLDQVTKLEKCFQDFNNHNYETHA	197
Query	205	GYPYCGMSFRLANMAAGNSEICYRRGKNDAKLFQMNIIDSGDAPQLCGAMHSDNIFAFPTP	264
		C + + AA N+E+C RR I++ + C + N+ TP	
Sbjct	198	LRSLCAVEVKSFMSAAVNTEVCMRRTNF-----INNLGGSKYCDPLEGRNVSPCTP	249

```
Query 265 IP--TSPTNETIITS-KYMMVTARMDSFSGMPEISVGEVSVLTSIISVLAAARSMGTQIE 321
      + T ET+ T+ K+++VT R+D+ M + +G + L A + ++
Sbjct 250 ESQQSETTLETVHTNEKFILVTCRLDTTTFDGVGLGAMDSLGMF---AVFTHVAYLLK 305

Query 322 KWQKASNTSNRNVFFAFFNGESLDYIGSGAAAYQMENGKFPQMIRSDRTHIHPIRPNELD 381
      + + NV F FNGES DYIGS Y ME +FP ++ T PI + +D
Sbjct 306 QLLPPQSKDLHNVLFVTFNGESYDYIGSQRFVYDMEKLQFP---TESTGTPPIAFDNID 361

Query 382 YILEVQQIGVAKGRKYYVHVDGERYQQNKTQTDRVIDRIERGLRS--HAFDLEKPSGSGD 439
      ++L++ + K + T ++++R+ +S + F+L S
Sbjct 362 FMLDIGTLDDISNIKLHA-----LNGTTLAQQILERLNNYAKSPRYGFNLNIQSEMSA 414

Query 440 RVPPASWHSFAKADAHVQSVLLAPYGKEYEYQRVNSILDKNEWTEDEREKAIQEIEAVST 499
      +PP S SF + D + +++L Y D ++T K ++ V+
Sbjct 415 HLPPTSAQSFLRRDPNFNALILNARPTNKYYHSTYDDADNVDFTYANTSKDFTQLTEVN- 473

Query 500 AILAAAADYVGVETDEVVAKV 520
      D+ + D + KV
Sbjct 474 -----DFKSLNPDSLQMKV 487
```

CPU time: 0.03 user secs. 0.01 sys. secs 0.04 total secs.